Figure S1

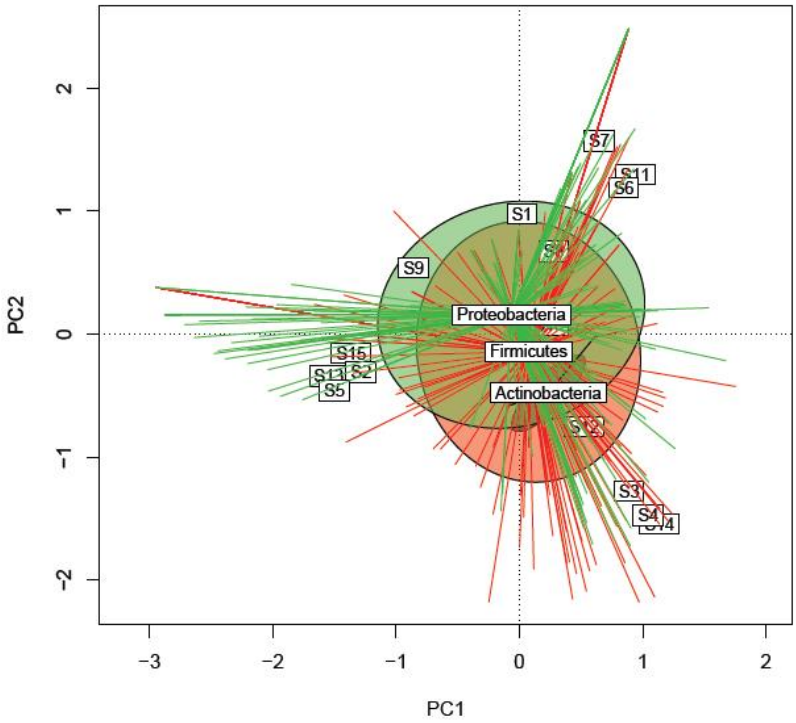

FIG S1. Principal component analysis results at the genus/species composition among samples from the human gut microbiota of athletes

Figure S2

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LRH      ------------MTASPWDLRKVLDELKQDPQQYHETDVQVDPDAELAGVYRYIGAGGTV
LPL      ------------MAEQPWDLRRVLDEIKDDPKNYHETDVEVDPNAELSGVYRYIGAGGTV
PET      -----------MAKKDVYDLRKVLDELKKEPGQYHETNVEVDPDAELSGVYRYIGAGGTV
ERA      -------------MSTPYDLRKVLAELQEMPGEYHETNVEVDPHAELSGVYRYIGAGGTV
SGA      ------------MSEQPYDLRKVLEELKEIPGQYHETDVEIDPNAEISGVYRYIGAGGTV
ECL      ------------MQNPINDLRSAIALLQRHPGHYIETDHPVDPNAELAGVYRHIGAGGTV
ACH      MEQP---FPAFIDFPPINDLRSALARLQQVPGQLLHTDHPVDPHGELAGVYKRVGAGGTV
KIN      -----MNRTDHTANSPVIDLRSALARLEQSPDELISTDHEIDPRSELAGVYKRVGAGGTV
ATR      MEDNVMDRTDHAANSPVIDLRSALARLEAFPGELISTDQEVDPRSELAGVYKRVGAGGTV
AGL      ------------MNDTIHDLRSALDYLRDMPGQLLETDTEVDCDAEVSGVYRHVGAGGTV
ERY      -------------MKEPYDLRSALQQLEAEEGQLLITDKLTNTDGELAGVYRYIGGGGTL
COP      -----------MSKKKVRDLRSALELLQSIDGQLVETDVEVDPLGELSGVYRHVGAGGTV
BLA      ------------MAEKVRDLRSALALLEQMPDQLIETEVEVDPMAELAGVYRYVGAGGTV
FIR      ------------MADKVRDLRSALERLKTMEGQYIETDVEVDPMAELAGVYRYVGAGGTV
AHA      ------------MQDKVRDLRSALKRLKQMEGQYIETDVEVDPMAELAGVYRYVGAGGTV
LAC      ------------MQDKVRDLRSALKRLKQMEGQYIETDVEVDPMAELAGVYRYVGAGGTV
DLO      ------------MAAKVTDLRSALKMLEDMPGQLIETDVEVEPMAELSGVYRHVGAGGTV
IBA      -------------MNKVRDLRSALELLENMPGQLIETDVEVDPMAELSGVYRHVGAGGTV
CBU      ------------MSNKVYDLRSALELLKTLPGQLIETDVEVDPMAELAGVYRYVGAGGTV
HHA      ---------------MVEDLRSAVEELKKYENQIACTDTEVDSYAEVAGIYRYVGAGGTV
TSA      ---MKIKERVNKMANQIHDLRSAIEFLKQHENQIVYTNSEVDCEAEISGIYRYVGAGGTV
PAG      ---------MSGKESKVNDLRSALALLSQYDNELIYTDEPVDPVAELSGVYRYVGAHGTV
HAL      ----MANNADNKIKNPIHDLRSALEFLKNQPGELVSTNVEVDPCAELSGVYRYVGAGGTC
SBL      --------MKNKDKIPVHDLRSALELLKTLPGEYVETFTEVDPHAELSGVYRYVGAGGTC
KRA      -----MSNSENKNTSGVTDLRSAIELLKTLPGEYVETDTEVDPHAELSGVYRYVGAGGTC
KMI      -----MANSDNKTPSSVHDLRSALELLKTLPGEYVETDTEVDPHAELSGVYRYVGAGGTC
                         *** .:  :     .   *    :  .*::*:*: :*. **
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LRH      ERPTQ-EGPAMMFNNVVGFPTTRVLIGLMASRKRVGKMFHQDYHTLGRFLNKAVLNPIQP
LPL      QRPTQ-EGPAMMFNNVKGFPDTRVLTGLMASRRRVGKMFHHDYQTLGQYLNEAVSNPVAP
PET      QRPTQ-EGPAMMFNNVKGFPDTRVLMGLMASRKRVGKMFHHDYHTLGQFLNDSVENPVDP
ERA      KRPTK-EGPAMMFNCVKGFPDTRVLIGIIASRDRVGKILHHDPKHLGRLLKDSVQNPVKP
SGA      ERPTQ-EGPAMTFNNIKGFPNVRVNIGTMASRKRVGHILHHDYKDLGHLLNKAVENPVKP
ECL      KRPTR-TGPAMMFNSVKGYPGSRILVGMHASRERAALLLGCVPSKLAQHVGQAVKNPVAP
ACH      KRPTR-LGPAMMFNHIKGYPDSRVLVGVMASRERVALLLDTTPDRLAERMGEAIEKAIDP
KIN      MRPTR-TGPAMMFENVKGYPGARVLVGLMAKRERVALLLDSRPEELGRRMGEAVLNGIAP
ATR      MRPTR-TGPAMMFENVKGYPGARVLVGLMAKRERVALLLDSKPEELGQRMGEAVLNGIAP
AGL      ARPTK-EGPAMVFNNVKGFDDAKVAIGLLSSRKRVAALLGMDEQYLGLQIGQKLAETIPP
ERY      QRPTQ-LGPAMLFTNIQNHPGSRVLIGLLGDRQRCASLLNTTSEQLPFLMNKAYSKRLDP
COP      MRPTQ-EGPAMIFNHVKGHPGARVAIGLLASRRRVGYLLDCEPQKLGFLLKDSVNNPIKP
BLA      KRPTK-EGPAMIFNRIKGHPDARVAIGLLASRKRVAALLDTQPENLGKMLCKSVENPIPP
FIR      KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKRVAALLDCKPEELGKKLYYSVDNPIPP
AHA      KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKHVAALLDCKPEELGKKLYHSVDNPIAP
LAC      KRPTK-EGPAMVFNNVKGHKDARVAIGVLASRKRVAALLDCKPEELGKKLYHSVDNPIAP
DLO      MRPTK-EGPAMIFNNVKGHPGARVAIGVLASRTRVGALLECDPKDLGKKLYHSVDNPIPP
IBA      QRPTK-EGPAMIFNNVKGHKDARVLIGLLASRKRVAALLGTEPEDLGKLLYRSVDNPIPP
CBU      QRPTK-EGPAMIFNNIKGHKDARVLIGLLASRRRVAALLDCEPENLGKLLYRSVDNPIAP
HHA      KRPTK-EGPALLFRNIKGFPDKQVLIGLLASRKRVGYLLDCPPDKLGFLLKDAAANPVMP
TSA      MRPTK-IGPAMLFNHVKDYEHSKVLIGLFASRERVGLMLGCEPDRLGFLLNDALNHPVDP
PAG      KRPTR-VGPAMVFNKIKGFNDMRVLIGLLSSRQRVARLFGTSPENLAFMLKDSVLNPIPP
HAL      QRPTRKNGPAMVFNKIKGFDDISVTIGLNGSRKRVGHFLNCAPERLGHLLKDSVKNAIQP
SBL      QRPTRKNGPAMVFHNIKGFRNTNVAIGLNGSRKRVGHFLNCAPEKLGFLLKDSVKHAIAP
KRA      QRPTRKNGPVMMFNKVKGFQDISVAIGLNGSRKRVSHFLNCAPEKLGHLLKDSVQNPIPP
KMI      QRPTRKNGPVMVFNKIKGFKDISVAIGLNGSRQRVSHFLQCEPAKLGHLLKDSVENAIAP
          ***:  **.: *  : ..    :  *  ..* : . ::      *   :     . : *
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LRH      VTVE-ESAAPAHEVVAKASDPDFDIRKLVAAPTNTPQDAGPYITCGVVLGSNMAK-TMTD
LPL      ETVA-EADAPAHDVVYKATDEGFDIRKLVAAPTNTPQDAGPYITVGVVFGSSMDK-SKSD
PET      VMVD-EADAPTHEVVHKSTDADFDIRKLVAAPTNTPRDAGPYITVGVVYGSNPDK-TMSD
ERA      VKVA-KTDAPAQEVIHLATDEGFDIRKILAAPTNTEYDAGPYITMGVVFGSDPEK-TMSD
SGA      VKVS-KDQAPAQEVVHLATDDDFDIRKLIAAPTNTEYDAGPYITTGLVYGSTPDK-SMSD
ECL      VVVP-ASQAPCQEQVFYADDPDFDLRKLLPAPTNTPIDAGPFFCLGLVLASDPEDTSLTD
ACH      VVVP-REQAPCQEIVHRAEDPGFDLRTLLPAPTNTDEDAGPFFCLGLVLGSDPEE-GHAD
KIN      VVLK-GQSAPCQEQIFRADDPHFDLRNLLPAPTNTEEDAGPYFCLGLLLGSDPDN-GHTD
ATR      VVFK-EGSAPCQEQVFRADDPNFDLRHLLPAPTNTEEDAGPYFCLGLLLGSDPDN-GHTD
AGL      APIAEGKHIDCQEVVHLATDPDFDLRRLVPAPTNTPEDAGPYVTMGLIAGHSPFN-SDTD
ERY      VVVA---KGICQEIVHHREDEGFDIRRLLPAIKATKEDAGPYITMGLCYASEPET-KESD
COP      VVIP-HEQAKCQEVKYFADDPDFDIRKLVPAPTNTLEDAGPYITLGMCYASSPET-GESD
BLA      VDLE-G-DAPCQQVVHKAADPDFDLYKLVPAPTNTPDDAGPYITLGMCYATHPDT-GVHD
FIR      VEYQ-G-APPCQQVVHKAEDPDFNLYDLVPAPTNTPDDAGPYITLGMCYATHPDT-GVHD
AHA      VEYQ-G-DAPCQQVVHKVEDPDFNLYDLVPAPTNTPDDAGPYITLGMCYATHPDT-GVHD
LAC      VEYQ-G-DAPCQQVVHKVEDPDFNLYDLVPAPTNTPDDAGPYITLGMCYATHPDT-GVHD
DLO      VLTE-EA-APCQEVVHKATDPDFDLYKLVPAPTNTPVDAGPYITLGMCYASHPDT-GVSD
IBA      VLTD--KTPLCQEVVHRATDEDFDLYKLVPAPTNTPDDAGPYITLGMCYASHPDT-GCSD
CBU      VLTD-AKLPLCQQVVHKATDPDFDLNKLVPAPTNTPDDAGPYITLGMCYASHPDT-KFSD
HHA      EFTE-SGDVPCQEEIHYASDEGFDIRKILPAPQNTEEDAGPYITMGMCYASDPVT-GDGD
TSA      IEIP-QAKAKCQEVVHLSTDEGFDIRKILPAPKNTLEDAGPYITMGLCYASDPDT-KAGD
PAG      IVIP-REHAVCQEVVHLATDPDFDILKILPTPTNTPEDAGPYFTLGMCYAADPET-GEHD
HAL      VTVS-ADKAVCQQVTHFAEDADFDLRKLLPAPTNTEEDAGPYITMGLCYASDPDT-HESD
SBL      VDVS-TGNAVCQEVVHLATDPDFDLRKLLPAPTNTEEDAGPYITMGLCYASDPQT-HESD
KRA      IL-T-KDNAVCQQVVHLASDTNFDLRKLLPAPTNTEEDAGPYITMGLCYASDPET-HESD
KMI      VM-A-QGAAVCQQVVHLASDADFDLRKLLPAPTNTEEDAGPYITMGLCYASDPET-HESD
                    ::      *  *::  :: :   *  ****:.  *:  .         *


LRH      VTIHRMVLEDKDTLGIYIMPGGRHIGHFAEEYEKANKPMPVTINIGLDPAITIGATFEPP
LPL      VTIHRMVLEDKDKLGIYIMPGGRHIGAFAEEYEKANKPMPITINIGLDPAITIGATFEPP
PET      VTIHRMVLEDKDKLGIYIMPGGRHIGKFAEEYEKMNKPMPITINIGLDPAITIGATFEPP
ERA      VTIHRMVLEDEDTIGMYIMPGGRHIGHFQKQYEALNKPMPITINIGLDPAISIGTTFEPP
SGA      VTIHRMVLEDKDTIGIYIMPGGRHIGAFLSEYQKLNKPMPITINIGLDPAILIGATFEPP
ECL      VTIHRLCVQERDELSMFLAAG-RHIEVFRKKAEAAGKPLPVTINMGLDPAIYIGACFEAP
ACH      VTIHRLCVQGRDRLSIFFAPD-RHIDKFRQKAEAAGKPLPVTINMGLDPAILIGSCFEAP
KIN      VTIHRLCVQGRDELSVFFAPG-RHIDAFRAKAEERGEALPITINMGLDPAIPIGACFEAP
ATR      VTIHRLCVQGRDELSVFFAPG-RHIDAFRAKAEERGEALPITINMGLDPAIPIGACFEAP
AGL      VTIHRLCIESKDTMGMWITPGSRHLGAFFEQWKEKGEDMPVTVSIGLDPAVYMCAGFEAP
ERY      VTIHRLCLQSKDEMTMFFTPGIRHLDVFRKKAEAKNKALPISISIGVDPAIEIAACFEPP
COP      VTIHRMCFQSKDEISIFLQPGARHIGYFRELAEAKGEALPISISIGVDPAIEIASCFEAP
BLA      VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEELGQRLPISISIGVDPAIEIGSCFEPP
FIR      VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEELGQKLPISISIGVDPAIEIGSCFEAP
AHA      VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEELGQKLPISISIGVDPAIEIGSCFEAP
LAC      VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEELGQKLPISISIGVDPAIEIGSCFEAP
DLO      VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEELGQRLPISISIGVDPAIEIGSCFEPP
IBA      VTIHRLCIQSKDELSIFFTPGARHIGAMAERAEQLGQKLPISISIGVDPAIEIGSCFEPP
CBU      VTIHRLCIQGKDELSIFFTPGARHIGAMAERAEELGQNLPISISIGVDPAIEIGSCFEPP
HHA      VTIHRLCLQSADEMTMFFTPGVRHLDAFREKAEREGVNLPISISIGVDPAIEIASCFEPP
TSA      ITIHRLCLQSKDELTMFFTPGVRHIDAFRKKAEGNQNNLPISISIGVDPAIYVTSCFEPP
PAG      VTIHRLCVQSKDEISMYFVPG-RHLDTFRQKAEAAGKPLPITISIGVDPAIEIGACFEPP
HAL      ITIHRLCVQSRDELSMWLTPG-RHIDAFRMKAEAQGKPLPISISIGVDPAIEIAACFEPP
SBL      ITIHRLCVQSKDELTMWLTPG-RHIDAFRIKAEAAGKALPISISIGVDPAIEVAACFEPP
KRA      ITIHRLCVQSRDELSMWLTPG-RHIDAFRMKAEAAGKPLPISISIGVDPAIEIAACFEPP
KMI      ITIHRLCVQSRDELSMWLTPG-RHIDAFRMKAEAAGQPLPISISIGVDPAIEIAACFEPP
         :****: .:  * : :::  . **:  :    :     :*:::.:*:***: : : ** *
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LRH      TTPLGYDELGVAGAIRQEPVQLVQAVTVDEKAIARSEFTLEGYIMPNTRIQEDINTHTGK
LPL      TTPFGYNELGVAGAIRNQAVQLVDGVTVDEKAIARSEYTLEGYIMPNERIQEDINTHTGK
PET      TTPLGYNELGVAGAIRQEPVQLVKGLTVDEKAIARSEYTLEGYIMPNERIQEDINTHTGK
ERA      TTPLGYNELWVAGALRQEPVQLVDGVAVDEVGIARSEFIIEAEILPHETIQEDINTNTGK
SGA      TTPLGYNELWVAGALRNEPVQLVDSIAVDEVGIARSEFIIEGEILPNETIQEDINTHTGH
ECL      TTPFGYNELGVAGALRQQPVELVQGVAVKEKAIARAEIIIEGELLPGVRVREDQHTNTGH
ACH      TTPLGYDELKIAGGLRGRPVELVEAVSIGQKAIARAEVVIEGEILPHERLREDINTDSGR
KIN      TTPLGFDELTVAGGLRGRAVELVDAVTVKERSIARAEIVIEGEILPGRRIREDVNTNTGH
ATR      TTPLGFDELTVAGGLRGRAVELVDAVTVKERSIARAEIVIEGEILPGRRIQEDVNTNTGH
AGL      TTPLGYNELQIAGGIRGRAVELAPALTVPETCIAHAEYVIEGYLSITDTVREDVNTNTGK
ERY      TTPLGFNELSIAGGIRNKPVELCKCVSIDEYAIAHSEYVIEGELLPGKRMREDQHTGLGK
COP      TTPLGYDELQVAGAIRNEPVELVECLTINERAIANAEYVIEGEILPGKRIREDIHSNTGK
BLA      TTPLGYDELSVAGALRKEPVELCKCLTVNERAIANAEYVIEGEVIPGVRVKEDQNSNTGY
FIR      TTPLGYDELAVAGALRNEPVELCKCLTVNEMAIANAEYVIEGEVILNVRVQEDQNSHTGY
AHA      TTPLGYDELSVAGALRNEPVELCKCLTVNEMAIANAEYVIEGEVIPNVRVQEDQNSHTGY
LAC      TTPLGYDELSVAGALRNEPVELCKCLTVNEMAIANAEYVIEGEVIPNVRVQEDQNSHTGY
DLO      TTPMGYDELAVAGALRGEPVRLCKCLTVNERAIANAEYVIEGEVVPNVRVQEDQNSHTGY
IBA      TTPMGYDELAVAGALRGEAVELCNCLTVNEKAIANAEYVIEGEVIPNVRVQEDQNSNTGY
CBU      TTPLGYDELSVAGALRGKPVELCKCITVNERAIANAEYVIEGEVIPNLRVQEDKNSNTGY
HHA      TTPLGFNELSIAGALRKKPVRMAKCRTIDEYAIANAEFVIEGELVAGKRMREDINTNTGK
TSA      ATPLGFNELSIAGGLRGKPVELTKCLTIDEMAIANAEYVIEGELVFGQRMREDINTNTGK
PAG      TTPLGFDELSVAGSLRNQAVELVDCLTVNARGIANAEIVIEGELVPNYRVREDQNTNTGK
HAL      TTPLGFDELSIAGALRGHAVEMVQCKTINEKAIAHAEIVIEGELLPNLRVREDQNTNTGK
SBL      TTPLGFNELSIAGALRGRAVEMVQCKTINEKAIAHAEIVIEGELLPDVRMQEDINTHTGR
KRA      TTPLGYDELSVAGALRGKAVEMVQCKTINERAIAHAEIVIEGELLPNVRLREDQNTNTGK
KMI      TTPLGFNELSIAGALRGKAVEMTQCKTINEKAIAHAEIVIEGELRPNARVREDQNTHTGR
         :**:*::** :**.:* . *.:    ::    **.:*  :*. :     ::** ::  *

LRH      AMPEFPGYDGDANPALQVIKVTAVTHRRDHPIMQSVIGPSEEHVSMAGIPTEASILQLVD
LPL      AMPEFPGYDGDANPALQVIKVTAVTHRK-NAIMQSVIGPSEEHVSMAGIPTEASILQLVN
PET      AMPEFPGYDGDANPALQVIKVTAVTHRK-DPIMQSVIGPSEEHVSMAGIPTEASILSLTN
ERA      AMPEFPGYNGDANPAVNVVKVKAITHRKDRPIMQTTIGPSEEHVSMAGIPTEASILDLVD
SGA      AMPEFPGYNGPANPALNVIKVKAVTHRKDNPIMQTTIGPSEEHVSMAGIPTEASILNLVD
ECL      AMPEFPGYCGEANPSLPVIKVKAVTMRN-HAILQTLVGPGEEHTTLAGLPTEASIRNAVE
ACH      AMPEFPGYTGPANPSLPVIRVTAVTMRR-QAILQTLVGPGEEHTNLAGIPTEASIRNAVE
KIN      AMPEFPGYNGPANPALPVIKVKAVTMRK-NAILQTLVGPGEEHVNLAGIPTEASIFNACD
ATR      AMPEFPGYNGPANPSLPVIKVTAVTMRK-NAILQTLVGPGEEHVNLAGIPTEASIFNACD
AGL      AMPEFPGYTGEAKPELPVIHVTAVTHRE-HPIMQSCIGPSHEHVSMAGIPTEASIYKMVE
ERY      AMPEFPGYCGEANPSLPVIRVKAITHRK-NPIMRVCLGPGEEHVNLAGIPTEASILSLCE
COP      AMPEFPGYCGPANPELPIIKVKAVTTRK-NPIMQTCIGPSEEHVSMAGIPTEASILTMVD
BLA      AMPEFPGYTGPASDQCWLIKVTAVTHRE-NPIMQTCIGPSEEHVSMAGIPTEASIYGMVE
FIR      AMPEFPGYTGPASSQCWLIKVKAVTHRE-NPIMQTCIGPSEEHVSMAGIPTEASIYGMVE
AHA      AMPEFPGYTGPASSQCWLIKVKAVTHRE-NPIMQTCIGPSEEHVSMAGIPTEASIYGMVE
LAC      AMPEFPGYTGPASSQCWLIKVKAVTHRE-NPIMQTCIGPSEEHVSMAGIPTEASIYGMVE
DLO      AMPEFPGYTGPASDQCWMIKVTAVTHRK-NPIMQTCIGPSEEHVSMAGIPTEASIYGMVE
IBA      AMPEFPGYTGPASDQCWMIKVTAVTHRK-NPIMQTCIGPSEEHVSMAGIPTEASIYGMVE
CBU      AMPEFPGYTGPASDQCWMIKVKAVTHRE-NPIMQTCIGPSEEHVSMAGIPTEASIYGMIE
HHA      AMPEFPGYTGHVSGELPVIKIKAVTHRK-NPMIQTCIGPSEEHVSMAGIPTEASILTMEE
TSA      AMPEFPGYTGVADQALPVIKVKAITHRK-NPIMQTCIGPSEEHVNLAGIPTEASILNMVE
PAG      AMPEFPGYTGAAQAEVPVIKVKAITHRR-HPILQTCIGPSDEHTNLAGIPTEASILQMIE
HAL      AMPEFPGYTGAAKDALPVIKVKAVTHRY-HPIWRTTIGPGEEHVNMAGIPTEASILDMVE
SBL      AMPEFPGYTGEAKAAIPVIKVKAVTHRV-NPIWRTTLGPGEEHVNMAGIPTEASILDMVE
KRA      AMPEFPGYTGEAKDALPVIKVKAVTHRY-NPIWRTTVGPGEEHVNMAGIPTEASILDMVG
KMI      AMPEFPGYTGEAKEAIPVIKVKAVTHRI-NPIWRTTVGPGEEHVNMAGIPTEASILDMVE
         ******** * ..    ::::.*:* *    : :  :**..**..:**:******
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```
LRH      RAIPGKVKNVYNPPAGGGKLMTIMQIHKDNPADEGIQRQAALLAFSAFKELKTVWLVDDD
LPL      RAIPGKVTNVYNPPAGGGKLMTIMQIHKDNEADEGIQRQAALLAFSAFKELKTVILVDED
PET      RAIPGKVLNVYNPPAGGGKLMTIMQIHKDNAADEGIQRQAALLAFSSFKELKTVFLVDED
ERA      KAIPGKVTNVYNPPAGGGKLMSILQIHKESEADEGIQRQAAILALSAFKELKTVILVDDD
SGA      KAIPGKVLNVYNPPAGGGKLMTIMQIRKENPADEGIQRQAALLAFSSFKELKTVILVDED
ECL      EAIPGFLQNVYAHTAGGGKFLGILQVKKRQPSDEGRQGQAALIALATYSELKNIILVDED
ACH      RAMPGLLKNVYAHTAGGGKLLAVLQVAKRRPGDEGRQRQAALIALAVYRELKNVILVDED
KIN      KALPGFVKNVYAHSAGGGKLLAILQVCQRSAGDVGKARQAALIALAVYRELKNVIIVDDD
ATR      KALPGFVKNVYAHSAGGGKLLAILQVCQRSAGDAGKARQAALIALAVYRELKNIIIVDDD
AGL      TAIPGRLLNVHAAPCGGGKFVAVLQFKKSSINDEGRQRNAAMLAFSAFSELKHVFLVDED
ERY      KAMPGNVRNVHCASSGGGKYIAVLQFVKRMESDEGRQRQAALLAFSAFSELKHVFLVDED
COP      KAMPGKLQNVYCASSGGGKYIAVMQFKKSVPSDEGRQRQAALLAFSAFAELKHVFLVDED
BLA      KAMPGRLQNVYCSSAGGGKYMAVLQFKKLSQSDEGRQRQAALLAFSAFSELKNVFLVDED
FIR      KAMPGRLQNVYCGSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHVFLVDED
AHA      KAMPGRLQNVYCGSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHVFLVDED
LAC      KAMPGRLQNVYCGSAGGGKYMAVLQFKKREASDEGRQRQAALLAFSAFSELKHVFLVDED
DLO      KAMPGRLQNVYCASPGGGKYMAVLQFKKLTASDEGRQRQAALLAFSAFSELKHVFLVDED
IBA      KAMPGRLQNVYCSSAGGGKYMAVLQFKKSVASDEGRQRQAALLAFSAFSELKNIFIVDED
CBU      KAMPGRLQNVYCCSSGGGKFMAVLQFKKTVASDEGRQRQAALLAFSAFSELKNIFLVDED
HHA      KALAGRVKNVYAHRSGGGKYMAVIQFAKQVPSDEGRQRQAALIALTAFPELKHVIVVDED
TSA      RAMPGRVLNVYAHSSGGGKYLAILQFKKSIPSDEGRQRQAALVAFSAFPELKHVILVDED
PAG      RALPGFVQNVHCPSPGTGKYLAVLQVKKRFAVDEGRQRQAALLAFSAFSELKHVMLVDED
HAL      RAMPGKLLNVFAHSAGGGKLLAVMQFKKSAPVDEGRQRQAALLAFSAFSELKHVILVDED
SBL      RAMPGKLLNVFAHSAGGGKLLAVMQFKKSSVNDEGRQRQAALLAFSAFPELKHVILVDED
KRA      RAMPGKLLNVFAHSAGGGKLLAVMQFKKFSPADEGRQRQAALLAFSAFPELKHVILVDED
KMI      RAMPGKLLNVFAHSAGGGKLLAVLQFKKSSPADEGRQRQAALLAFSAFPELKHVILVDED
          *: * : **.    * ** : ::*. :    * *   :**::*:: : *** : :**:*

LRH      VDIFDMNDVVWTMNTRFQGDQDIMVLPGMRNHPLDPSERPQYDPKSIRVRGMSSKTVIDG
LPL      VDIFDMNDVIWTMNTRFQADQDLMVLSGMRNHPLDPSERPQYDPKSIRFRGMSSKLVIDG
PET      VDIFDMNDVVWTINTRFQADQDIMVLPGMRNHPLDPSERPEYDPKSIRTRGMSSKLVIDG
ERA      VDIFDMNDVMWTLNTRFQGDQDILVLPGMRNHPLDPSERPEYDPKSIRFRGMSSKTILDG
SGA      VDIFDMNDVMWTINTRFQAHKDIMSLEGMRNHPLDPSERPEYSPEHIRVRGMSSKLVLDG
ECL      VDIFDSDDILWAMTTRMQGDVSITTLPGIRGHQLDPSQSPDYST-SIRGNGISCKTIFDC
ACH      VDPFDSDDVLWAMQTRYQGDVDTIFVPGVPGHVLDPSQVPEYSP-SIAARGLTCKTIFDC
KIN      VDLFDSNDVLWAMQTRYQGNVDTMFLPGVTGHVLDPSQVPEYDP-SIPAKGVSCKTIFDC
ATR      VDLFDSNDVLWAMQTRYQGNVDTMFLPGVTGHVLDPSQVPDYDP-SIPAKGVSCKTIFDC
AGL      VDIFDMSDVMWAMTTRFQADTGLITIPGAHCHVLDPSNDPAFAP-SIRVHGIACKAIFDC
ERY      VDIYDMKDVLWAMTTRFQSDIDCISIPGVRCHPLDPSNDTTYDP-SIRDRGIACKTIFDC
COP      VDPFDMKDVMWAMTTRFQADLDLITIPGVQCHPLDPSNQPEYSA-HIRARGVACKAIFDC
BLA      VDCFDMNDVLWAMNTRFQGDVDVITIPGVRCHPLDPSNDPAFSP-SIRDHGIACKTIFDC
FIR      VDCFDMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSP-SIRDHGIACKTIFDC
AHA      VDCFDMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSS-SIRDHGIACKTIFDC
LAC      VDCFDMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPTCSS-SIRDHGIACKTIFDC
DLO      VDCFDMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPSCSG-SIRDHGIACKTIFDC
IBA      VDCFDMNDVLWAMNTRFQGDVDVITIPGVRCHPLDPSNDPSFSP-SIRDHGIACKTIFDC
CBU      VDCFDMNDVLWAMNTRFQGDADIITIPGVRCHPLDPSNDPDYSP-SIKNHGIACKTIFDC
HHA      VDIFDSDDVLWALNTRYQGDVDTITIPGVRCHPLDPTEGPEYNP-MLKDRGISCKTIFDC
TSA      VDIFDSNDVLWALTTRYQGDLDTVFIPGVRCHPLDPSSSNLYHP-SILSTGIACKTIYDC
PAG      VDVFDLSDVMWAMTTRYQGDVSTVFIPGVRCHPLDPSSDPAFSP-SVRDHGITCKTIFDC
HAL      VDIFDSDDVMWAMQTRYQGDVDTVFIPGVRCHPLDPSQMPDYSP-SILQEGMSCKTIFDC
SBL      VDIFDTDDVLWAMQTRYQGDIDTITIPGVRCHPLDPSQVPEYSP-FITQQGMTCKTIFDC
KRA      VDIFDSDDVLWAMQTRYQGDVDTVTIPGVRCHPLDPSQIPAYSP-SILQQGMSCKTLFDC
KMI      VDIFDSDDVLWAMQTRYQGDVDTIVIPGVRCHPLDPSQVPEYSP-SILQQGMSCKTIFDC
         ** :* .*::*:: ** *.. .   : *   * ***:.        :   *::.* : *
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LRH      TVPFDMRDQFKRAAFKKVS--DWQKYLK-----
LPL      TVPFDMKDQFERAQFMKVA--DWEKYLK-----
PET      TVPFDMKDQFERAQFKEVK--DWEKYLK-----
ERA      TVPFDLKDDFIRAEFKEVP--DWEKYLK-----
SGA      TVPFDMKDQFERAKFKEVP--DWKKYLD-----
ECL      TVPWALKARFERAPFMEVDPTPWAPELFSDKK-
ACH      TAPWHLRERFERAKFRDVDPHPFAPELFPQARS
KIN      TYPWKLKEHFVRAQFRDVDPHPFAPSIFPKAGM
ATR      TYPWKLKEHFVRAQFREVDPHPFAPSIFPKAGM
AGL      TVPYDLKDEFQRCRFLDIDQDKWAAELAH----
ERY      TVPFSQKERFQRAAFQEVEASQWLK--------
COP      TVPFDQKARFERAKFMDVDPKCWLPDMLK----
BLA      TVPYDLKEDFHRARFMELDPEKWLKK-------
FIR      TVPYDQKERFKRARFMEVDPEHWL---------
AHA      TVPYDQKERFKRARFMEVDPEHWLS--------
LAC      TVPYDQKERFKRARFMEVDPEHWLS--------
DLO      TVPYDQKDRFKRAQFMDVDPEHWVK--------
IBA      TVPFEQKERFKRARFMDVDPEHWLKDIK-----
CBU      TVPFHMKERFKRAKFMEVDPEHWL---------
HHA      TVPYGLKDRFQRSKFKEVNMEDYEIRPLV----
TSA      TVPFIQKERFKRSSFKEVNLSDYDIKPLK----
PAG      TVPYNLKANFHRSEFLEVDVNRFIPGFNQK---
HAL      TVPFHLKAHFERSRFKEADVKRFLPDFE-----
SBL      TVPFHLKTHFERSTFKEVDVKRFLPDFE-----
KRA      TVPFHLKSHFERSKFKEVDVKRFLPDFE-----
KMI      TVPFHLKHTFQRSRFKEVDVKRFLPDFE-----
         * *:  :  * *. * .     :
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FIG S2. Comparison of amino acid sequences of subunit C of putative gallate decarboxylase proteins from bacteria identified by HTS from athlete faecal microbiota. Multiple alignments were done using the programs ClustalOmega after retrieval of sequences from BLAST homology searches. The C subunits are from *Acetobacter tropicalis* (ATR) (WP_006559787.1), *Actinomyces glycerinitolerans* (AGL) (WP_073329259.1), *Anaerostipes hadrus* (AHA) (WP_009204323.1), *Azotobacter chroococcum* (ACH) (WP_052264016.1), *Blautia* sp. KLE 1732 (BLA) (WP_021650680.1), *Clostridium butyricum* (CBU) (WP_058371993.1), *Coprobacillus* (COP) (WP_008787659.1), *Dorea longicatena CAG:42* (DLO) (CDE20644.1), *Enterobacter cloacae* subsp. *cloacae* ATCC 13047 (ECL) (YP_003612445.1), *Enterococcus* (ERA) (WP_010743655.1), *Erysipelotrichaceae* bacterium 3_1_53 (ERY) (EFP59895.1), Firmicutes bacterium CAG:270 (FIR) (CDD72954), *Hafnia*

alvei ATCC 51873 (HAL) (WP_004092226.1), *Hungatella hathewayi* (HHA) (WP_006771947.1), *Intestinibacter bartlettii* (IBA) (WP_007285641.1), *Klebsiella michiganensis* KCTC 1686 (KMI) (AEX02211.1), *Komagataeibacter intermedius* (KIN) (WP_039733191.1), *Kosakonia* (KRA) (WP_071921386.1), *Lachnospiraceae* bacterium 5_163FAA (LAC) (EFV16561), *Lactobacillus rhamnosus* (LRH) (WP_005712295.1), *Lactobacillus plantarum* ATCC 14917T (LPL) (D7VDD5), *Pantoea agglomerans* strain FDAARGOS_160 (PAG) (AMG60167.1), *Pediococcus ethanolidurans* (PET) (WP_057806460.1), *Shimwellia blattae* (SBL) (WP_002441866.1), *Streptococcus* (SGA) (WP_003065832.1), and *Turicibacter sanguinis* (TSA) (WP_040763984.1). Residues that are identical (*), conserved (:) or semiconserved (.) in all sequences are indicated. Dashes indicated gaps introduced to maximize similarities. Degenerate primers were designed on the conserved domains highlighted.